

Figure 2B. The cDNA (SEQ ID. NO:4) and amino acid sequence (SEQ ID. NO:5) of 121P1F1 splice variant 1A. The start methionine is underlined. The open reading frame extends from nucleic acid 82-462 including the stop codon.

```

1 ccaaaatcaaaegcgctcgggcctgtccgcgccctctcccaagcgcgggcccgccagc
1      M S K K K G L S A E E K R
61 ggaagccctgcgcccgcgccATGTCAAAGAAAAAGGACTGAGTGCAGAAGAAAAGAGA
14 T R M M E I F S E T K D V F Q L K D L E
121 ACTCGCATGATGGAATATTTTCTGAAACAAAAGATGTATTTCAATTAAGACTTGGAG
34 K I A P K E K G I T A M S V K E V L Q S
181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAGAAGTCCCTCAAAGC
54 L V D D G M V D C E R I G T S N Y Y W A
241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACCTCTAATTATTATTGGGCT
74 F P S K A L H A R K H K L E V L E S Q D
301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGGAC
94 P G C C F H E I I K V S Y Y R K F W L G
361 CCTGGCTGCTGCTCCATGAAATAATTAAAGTCTCCTATTATAGAAAATTCTGGCTGGGC
114 A V A H A C N P S T L G G *
421 GCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAggcgggcagatcacgagg
481 tgactttccccccacccccacatgaagtgaagatggagttgtctgaggggaagtcaaaagc
541 atgcaagcctacagaaaagcattgagaaagctaaaattggcagatgtgaaacggaagagc
601 gaaccaggctagcaaaagagctttcttcacttcgagaccaagggaacagctaaaaggcag
661 aagtagaaaaatacaaaagactgtgatccgcaagttgtggaagaaatacgcgaagcaaata
721 aagttagcaaaagaagctgtgtaacagatggactgataacataattcgcaataaaatcttggg
781 ccaaaaagaaaatttgggtttgagagaaaataaaattgtagaacttttggaattccagaag
841 actttgactacatagactaaaatattccatggtggtgaaggatgtacaagcttgtgaata
901 tgtaaaatttaaaactattatctaactaagtgtactgaattgtcggttgctctgaactgtg
961 ttatcattttattaatgttaataaagtgtaaaaatgcaaaaaaaaaaaaaaaaaaaaaa
1021 aaaaaaaa

```

Figure 2C. The cDNA (SEQ ID. NO:6) and amino acid sequence (SEQ ID.NO:7) of 121P1F1 splice variant 1B. The start methionine is underlined. The open reading frame extends from nucleic acid 501-860 including the stop codon.

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1  ccaaaatcaaaacgcgtccggcctgtcccgccctctcccaagcgcgggcccggccagc
61  ggaagcccttgcccgccgcatgtcaaagaaaaaggactgagtcagaagaaaaagaga
121 actcgcatgatggaatatatttctgaacaaaagatgtatttcaattaaaagacttggag
181 aagattgctcccaagagaaaaggcattactgctatgtcagtaaaagaagtctctcaaacg
241 ttagtgtgatggtatggttgactgtgagaggatcggaacttctaattattattgggct
301 ttccaagtaaagctcttcatgcaaggaaacataagttggagggttctggaatctcaggac
361 cctggctgctgcttccatgaaataaataaagctctcctattatagaaaattctggctgggc
421 gcagtggtcaccgcctgtaatcccgagcactttgggaggctgaggcgggcagatcacgagg
1      M K C K M E L S E G S Q K H
481 tgactttccccacccccacATGAAGTGAAGATGGAGTTGTCTGAGGGAAGTCAAAAGC
15   A S L Q K S I E K A K I G R C E T E E R
541 ATGCAAGCTACAGAAAAGCATTGAGAAAGCTAAAATTGGCCGATGTGAAACGGAAGAGC
35   T R L A K E L S S L R D Q R E Q L K A E
601 GAACCAGGCTAGCAAAAGAGCTTTCTTCACTTCGAGACCAAGGGAACAGCTAAAGGCAG
55   V E K Y K D C D P Q V V E E I R Q A N K
661 AAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGGAAGAAATACGCCAAGCAATA
75   V A K E A A N R W T D N I F A I K S W A
721 AAGTAGCCAAAGAAGCTGCTAACAGATGGACTGATAACATATTTCGAATAAAATCTTGGG
95   K R K F G F E E N K I D R T F G I P E D
781 CCAAAAGAAAATTTGGGTTTGAAGAAAAATAAATTTGATAGAACTTTTGAATTCAGAAG
115   F D Y I D *
841 ACTTTGACTACATAGACTAAaattatccatggtggtgaaggatgtacaagcttgtgaata
901 tgtaaattttaaactattatctaactaagtgactgaattgtcggttgcctgtaactgtg
961 tttatcattttattaatgttaaataaagtgtaaaatgcaaaaaaaaaaaaaaaaaaaaaa
1021 aaaaaaaa

```

Figure 2D. The cDNA (SEQ ID. NO:8) and amino acid sequence (SEQ ID. NO:9) of 121P1F1 splice variant 2. The start methionine is underlined. The open reading frame extends from nucleic acid 82-450 including the stop codon.

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1 ccaaaatcaaacgcgtccgggcctgtcccgccctctccccaagcggggcccgccagc
1      M S K K K G L S A E E K R
61 ggaagcccctgcgcccgcgccATGTCAAAGAAAAAGGACTGAGTGCAGAAAGAAAGAGA
14 T R M M E I F S E T K D V F Q L K D L E
121 ACTCGCATGATGGAATATTTTCTGAAACAAAAGATGTATTCAATTAAGACTTGGAG
34 K I A P K E K G I T A M S V K E V L Q S
181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAGAAGTCCCTCAAAGC
54 L V D D G M V D C E R I G T S N Y Y W A
241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAATTCTAATTATTATGGGCT
74 F P S K A L H A R K H K L E V L E S Q L
301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGTTG
94 S E G S Q K H A S L Q K S I E K A K I G
361 TCTGAGGGAAGTCAAAGCATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGC
114 R C E T A K Q I K *
421 CGATGTGAAACGGCCAAGCAATAAAGTAGCcaagaagctgctaacagatggactgata
481 acatatctgcaataaaaatcttgggccaagaaaatttgggtttgaagaaaaataaaattg
541 atagaacttttggaaattccagaagactttgactacatagactaaaatattccatggtggt
601 gaaggatgtacaagcttgtgaatatgtaaaattttaaactattatctaactaagtgtactg
661 aattgtcgtttgcctgtaactgtgtttatcattttattaatgttaataaaagtgtaaaa
721 gcaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
    
```

Figure 2E. The cDNA (SEQ ID. NO:10) and amino acid sequence (SEQ ID. NO:11) of 121P1F1 splice variant 3. The start methionine is underlined. The open reading frame extends from nucleic acid 82-654 including the stop codon.

```

1 ccaaaatcaaacgcgtccggcgctgtccgcgccctctcccaagcgcgggcccggccagc
1      M S K K K G L S A E E K R
61 ggaagccctgcgcgcgcgcATGTCAAAGAAAAAGGACTGAGTGCAGAGAAAAAGAGA
14 T R M M E I F S E T K D V F Q L K D L E
121 ACTCGCATGATGGAATATTTTCTGAAACAAAAGATGTATTTCAATTAAGAGACTTGGAG
34 K I A P K E K G I T A M S V K E V L Q S
181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAGAAGTCCCTCAAAGC
54 L V D D G M V D C E R I G T S N Y Y W A
241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACCTCTAATTATTATTGGGCT
74 F P S K A L H A R K H K L E V L E S Q L
301 TTTCCAAGTAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGTTG
94 S E G S Q K H A S L Q K S I E K A K I G
361 TCTGAGGGAAGTCAAAAGCATGCAAGCCTACAGAAAGCATTGAGAAAGCTAAAATTGGC
114 R C E T E E R T R L A K E L S S L R D Q
421 CGATGTGAACGGAAGAGCGAACCAGGCTAGCAAAAGAGCTTTCTTCACTTCGAGACCAA
134 R E Q L K A E V E K Y K D C D P Q V V E
481 AGGGAACAGCTAAAGGCAGAAAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGGAA
154 E I H N I F A I K S W A K R K F G F E E
541 GAAATACATAACATATTCGCAATAAAATCTTGGGCCAAAAGAAAATTTGGGTTTGAAGAA
174 N K I D R T F G I P E D F D Y I D *
601 AATAAAATTGATAGAACTTTTGAATCCAGAAGACTTTGACTACATAGACTAAaatatt
661 ccattggtggaaggatgtacaagcttgtgaatatgtaatttttaactattatctaact
721 aagtgtactgaattgtcggttgcctgtaactgtgtttatcatcttttattaatgttaataa
781 agtgtaaaatgcaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
  
```

Figure 2F. The cDNA (SEQ ID. NO:12) and amino acid sequence (SEQ ID. NO:13) of 121P1F1 splice variant 4. The start methionine is underlined. The open reading frame extends from nucleic acid 281-853 including the stop codon.

```

1  gttttctgtattgtaatatgtagagcacattccagaactgctcagtttcgagttaccta
61  tggatcttcaactgtgtgccaaattagtcgatttctgtgaaaacgccccggttcttgc
121  gggcaggagtcgctgctcttgtgccgggtgctgctggttgtgtaggcgctgttgc
181  ttaaggacgctctgcactgaattaggcttctcgtgggtcatgatcagttaaagtcctgtc
1
1      M M E I F S E
241  aaagaaaaaaggactgagtgcagaagaaagagaactcgcATGATGGAAATATTTTCTGA
8   T K D V F Q L K D L E K I A P K E K G I
301  AACAAAGATGTATTTCAATTAAGAACTTGGAGAAGATTGCTCCCAAAGAGAAAGGCAT
28  T A M S V K E V L Q S L V D D G M V D C
361  TACTGCTATGTCAGTAAAAGAAGTCTTCAAAGCTTAGTTGATGGTATGGTTGACTG
48  E R I G T S N Y Y W A F P S K A L H A R
421  TGAGAGGATCGGAACCTCTAATTATTATTGGGCTTTCCAAGTAAAGCTCTTCATGCAAG
68  K H K L E V L E S Q L S E G S Q K H A S
481  GAAACATAAGTTGGAGGTTCTGGAATCTCAGTTGTCTGAGGGAAGTCAAAGCATGCAAG
88  L Q K S I E K A K I G R C E T E E R T R
541  CCTACAGAAAAGCATTTGAGAAAGCTAAAATTGGCCGATGTGAAACGGAAGAGCGAACCGAG
108  L A K E L S S L R D Q R E Q L K A E V E
601  GCTAGCAAAGAGCTTTCTTCACTTCGAGACCAAGGGAACAGCTAAAGGCAGAAGTAGA
128  K Y K D C D P Q V V E E I R Q A N K V A
661  AAAATACAAAGACTGTGATCCGCAAGTTGTGGAAGAAATACGCCAAGCAATAAAGTAGC
148  K E A A N R W T D N I F A I K S W A K R
721  CAAAGAAGCTGCTAACAGATGGACTGATAACATATTCGCAATAAAATCTTTGGGCCAAAAG
168  K F G F E E N K I D R T F G I P E D F D
781  AAAATTGGGTTTGAAGAAAATAAAATTGATAGAACTTTTGAATTCAGAAAGACTTTGA
188  Y I D *
841  CTACATAGACTAAaatattccatgggtggtgaaggatgtacaagcttctgtaatatgtaaat
901  tttaaactattatctaactaagtgactgaattgtcggtttgctgtgaactgtgtttatca
961  ttttattaatgttaaataaaagtgtaaaatgcagatgttcttcaccccttttggtagaaca
1021  aaagcaggatgataaccatatccccccagtgctcatcaaagtaggacactaaaaatccat
1081  ccatctcagtcgaaagtcgagcgccgcgaatttagtagtagtagcggccgctctagagga
1141  tccaagcttacgtacgcgtgcatgacgcatagctcttctatagtgacacctaattc
1201  aagtt

```

Figure 3:

Figure 3A. Amino acid sequence of 121P1F1 (SEQ ID. NO:14). The 121P1F1 protein has 205 amino acids.

```

1  MSKKKGLSAE  EKTRRMMEIF  SETKDVFQLK  DLEKIAPKEK  GITAMSVKEV  LQSLVDDGMV
61  DCERIGTSNY  YWAFPSKALH  ARKHKLEVLE  SQLSEGSQKH  ASLQKSIEKA  KIGRCETEER
121  TRLAKELSSL  RDQREQLKAE  VEKYKDCDPQ  VVEEIRQANK  VAKEAANRWT  DNIFAIKSWA
181  KRKFGFEENK  IDRTFGIPED  FDYID

```

Figure 3B. Amino acid sequence of 121P1F1 splice variant 1A (SEQ ID. NO:15). The 121P1F1 splice variant 1A protein has 126 amino acids.

```

1  MSKKKGLSAE  EKTRRMMEIF  SETKDVFQLK  DLEKIAPKEK  GITAMSVKEV  LQSLVDDGMV
61  DCERIGTSNY  YWAFPSKALH  ARKHKLEVLE  SQDPGCCFHE  IIKVSYRKF  WLGAHAACN
121  PSTLGG

```

Figure 3C. Amino acid sequence of 121P1F1 splice variant 1B (SEQ ID. NO:16). The 121P1F1 splice variant 1B protein has 119 amino acids.

```

1  MKCKMELSEG  SQKHASLQKS  IEKAKIGRCE  TEERTRLAKE  LSSLRDQREQ  LKAEVEKYKD
61  CDPQVVEEIR  QANKVAKEAA  NRWTDNIFAI  KSWAKRKFGF  EENKIDRTFG  IPEDFDYID

```

Figure 3D. Amino acid sequence of 121P1F1 splice variant 2 (SEQ ID. NO:17). The 121P1F1 splice variant 2 protein has 122 amino acids.

```

1  MSKKKGLSAE  EKTRRMMEIF  SETKDVFQLK  DLEKIAPKEK  GITAMSVKEV  LQSLVDDGMV
61  DCERIGTSNY  YWAFPSKALH  ARKHKLEVLE  SQLSEGSQKH  ASLQKSIEKA  KIGRCETAKQ
121  IK

```

Figure 3E. Amino acid sequence of 121P1F1 splice variant 3 (SEQ ID. NO:18). The 121P1F1 splice variant 3 protein has 190 amino acids.

```
1  MSKKKGLSAE  EKRTRMMEIF  SETKDVFLQK  DLEKIAPKEK  GITAMSVKEV  LQSLVDDGMV
61  DCEIRIGTSNY  YWAFPSKALH  ARKHKLEVLE  SQLSEGSQKH  ASLQKSIEKA  KIGRCETEER
121  TRLAKELSSL  RDQREQLKAE  VEKYKCCDPQ  VVEEIHNIFA  IKSWAKRKFG  FEENKIDRTF
181  GIPEDFDYID
```

Figure 3F. Amino acid sequence of 121P1F1 splice variant 4 (SEQ ID. NO:19). The 121P1F1 splice variant 4 protein has 190 amino acids.

```
1  MMEIFSETKD  VFQLKDLEKI  APKEKGITAM  SVKEVLQSLV  DGMVDCERI  GTSNYYWAFP
61  SKALHARKHK  LEVLESQLE  GSQKHASLQK  SIEKAKIGRC  ETEERTRAK  ELSSLRDQRE
121  QLKAEVEKYK  DCDPQVVEEI  RQANKVAKEA  ANRWTDNIFA  IKSWAKRKFG  FEENKIDRTF
181  GIPEDFDYID
```


Figure 4A

Amino Acid Alignments.

Alignment of 121P1F1 protein and its variants.

A) CLUSTAL W alignment of 121P1F1 and variants 1-3. (SEQ ID NOS: 3, 5, 7, 9 and 11)

```

121P1F01 -----MSKKKGLSAEEKRTRMMEIFSETKDVFLKDKLEKIAPKEKGITAMSVKE
sv1A -----MSKKKGLSAEEKRTRMMEIFSETKDVFLKDKLEKIAPKEKGITAMSVKE
sv1B -----MKCKMELSEGSQKHAASLQKSIKAKIGRCETEERTRLAKESSLRDQRE
sv-2 -----MSKKKGLSAEEKRTRMMEIFSETKDVFLKDKLEKIAPKEKGITAMSVKE
sv-3 -----MSKKKGLSAEEKRTRMMEIFSETKDVFLKDKLEKIAPKEKGITAMSVKE

121P1F01 VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLELVESQLSEGSQK-HASLQKS-I
sv1A VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLELVESQDP-GCCF-HEIIKVSYY
sv1B QLKAEVEK-YKDCDPQVVEIRQANKVAKEAANRWTDNI FAIKSWAKRKFGFEENKID--
sv-2 VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLELVESQLSEGSQK-HASLQKS-I
sv-3 VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLELVESQLSEGSQK-HASLQKS-I

121P1F01 EKAKIGRCETEERTRLAKESSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKEAAN
sv1A RKFWLGAVAHACNPSTLGG-----
sv1B RTFGIPEDFDYID-----
sv-2 EKAKIGRCETAKQIK-----
sv-3 EKAKIGRCETEERTRLAKESSLRDQREQLKAEVEKYKDCDPQVVEIHNIFAISWAKR

121P1F01 RWTDNIFAISWAKRKFGFEENKIDRTFGIPEDFDYID
sv1A -----
sv1B -----
sv-2 -----
sv-3 KFGFEENKIDRTFGIPEDFDYID-----
  
```

Figure 4B

B) Clustal alignment of 121P1F1 and variants 1A and 4 (SEQ ID NOS 3, 13 and 5)

```

      1      15 16      30 31      45 46      60 61      75 76      90
1 121P1F01 MSKKKGLSAEEKRTR MMEIFSETKDVFLK DLEKIAPKEKGITAM SVKEVLQSLVDDGMV DCEIRIGTSNYYWAF PSKALHARKHKLEVL
2 sv-4 ----- MMEIFSETKDVFLK DLEKIAPKEKGITAM SVKEVLQSLVDDGMV DCEIRIGTSNYYWAF PSKALHARKHKLEVL
3 sv-1A MSKKKGLSAEEKRTR MMEIFSETKDVFLK DLEKIAPKEKGITAM SVKEVLQSLVDDGMV DCEIRIGTSNYYWAF PSKALHARKHKLEVL
-
      91      105 106      120 121      135 136      150 151      165 166      180
1 121P1F01 SOLSEGSQKHAASLQK SIEKAKIGRCETEER TRLAKESSLRDQRE QLKAEVEKYKDCDPQ VVEIRQANKVAKEA ANRWTDNI FAIKSWA
2 sv-4 SOLSEGSQKHAASLQK SIEKAKIGRCETEER TRLAKESSLRDQRE QLKAEVEKYKDCDPQ VVEIRQANKVAKEA ANRWTDNI FAIKSWA
3 sv-1A SQDPGCCHEIHKVS YRKKFWLG----- AVAHACNPS TLGG-----
-
      181      195 196      210 211
1 121P1F01 KRKFGFEENKIDRTF GIPEDFDYID 205
2 sv-4 KRKFGFEENKIDRTF GIPEDFDYID 190
3 sv-1A ----- 126
  
```

Figure 4C

C) Alignment of 121P1F1 and variant 1 (SEQ ID NO:20) with human GAJ (SEQ ID NO:21)
 Identities = 205/205 (100%), Positives = 205/205 (100%)

```

121P1: 1  MSKKKGLSAEEKRTRMMEIFSETKDVFLKDLKLEIAPKEKGITAMSVKEVLQSLVDDGMV 60
          MSKKKGLSAEEKRTRMMEIFSETKDVFLKDLKLEIAPKEKGITAMSVKEVLQSLVDDGMV
Sbjct: 1  MSKKKGLSAEEKRTRMMEIFSETKDVFLKDLKLEIAPKEKGITAMSVKEVLQSLVDDGMV 60

121P1: 61  DCEIRIGTSNYYWAFPSKALHARKHKLEVLESQLESGSQKHASLQKSIEKAKIGRCETEER 120
          DCEIRIGTSNYYWAFPSKALHARKHKLEVLESQLESGSQKHASLQKSIEKAKIGRCETEER
Sbjct: 61  DCEIRIGTSNYYWAFPSKALHARKHKLEVLESQLESGSQKHASLQKSIEKAKIGRCETEER 120

121P1: 121  TRLAKELSSLRDQREQLKAEVEKYKCDPQVVEEIRQANKVAKEAANRWTDNIFAISWA 180
          TRLAKELSSLRDQREQLKAEVEKYKCDPQVVEEIRQANKVAKEAANRWTDNIFAISWA
Sbjct: 121  TRLAKELSSLRDQREQLKAEVEKYKCDPQVVEEIRQANKVAKEAANRWTDNIFAISWA 180

121P1: 181  KRKFGFEENKIDRTFGIPEDFDYID 205
          KRKFGFEENKIDRTFGIPEDFDYID
Sbjct: 181  KRKFGFEENKIDRTFGIPEDFDYID 205
  
```

Figure 4D

D) Alignment of 121P1F1 and variant 1 (SEQ ID NO:22) with closest mouse homolog, a hypothetical 24.2 KDa protein. (SEQ ID NO:23)

Identities = 183/205 (89%), Positives = 193/205 (93%)

```

121P1: 1  MSKKKGLSAEEKRTRMMEIFSETKDVFLKDKLEKIAPKEKGITAMSVKEVLQSLVDDGMV 60
      MSKK+GLS  EEKRTMMEIF  ETKDVFLKDKLEK+APKEKGITAMSVKEVLQSLVDDGMV
Sbjct: 1  MSKKRGLSGEEKRTRMMEIFFETKDVFLKDKLEKLAPKEKGITAMSVKEVLQSLVDDGMV 60

121P1: 61  DCERIGTSNYYWAFPSKALHARKHKLEVLSQLSEGSQKHASLQKSIEKAKIGRCETEER 120
      DCERIGTSNYYWAFPSKALHARK  KLE  L  SQLSEGSQKHA  LQKSIEKA++GR  ETEER
Sbjct: 61  DCERIGTSNYYWAFPSKALHARKRKLEALNSQLSEGSQKHADLQKSIEKARVGRQETEER 120

121P1: 121  TRLAKELSSLRDQREQLKAEVEKYKCDPQVVEEIRQANKVAKEAANRWTDNIFAISWA 180
      LAKEL  S  RDQR+QLKAEVEKY++CDPQVVEEIR+ANKVAKEAANRWTDNIFAISWA
Sbjct: 121  AMLAKELFSFRDQRQLKAEVEKYRECDPQVVEEIREANKVAKEAANRWTDNIFAISWA 180

121P1: 181  KRKFGFEENKIDRTFGIPEDFDYID 205
      KRKFGFEE+KID+  FGIPEDFDYID
Sbjct: 181  KRKFGFEESKIDKNFGIPEDFDYID 205
    
```

Figure 4E

E) Alignment of 121P1F1 and variant 1 (SEQ ID NO:24)

with>gi|1175412|sp|Q09739|YA53_SCHPO HYPOTHETICAL 24.2 KD
 PROTEIN C13A11.03 IN CHROMOSOME I (SEQ ID NO:25)

gi|7490680|pir||T37610 hypothetical coiled-coil protein -
 fission yeast

(Schizosaccharomyces pombe)

gi|984224|emb|CAA90804.1| (Z54096) hypothetical coiled-coil
 protein [Schizosaccharomyces pombe]

Length = 210

Score = 121 bits (305), Expect = 5e-27

Identities = 81/202 (40%), Positives = 115/202 (56%), Gaps =
 6/202 (2%)

Query: 5

KGLSAEEKRTRMMEIFSETKDVFLKDLKLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCER 64

KGLS EKR R+ IF ++KD FQLK++EK+ K K I

+VK+VLQSLVDD +V E+

Sbjct: 4 KGLSLAEKRRRLEAIFHDSKDFFLKLEKEVKLGSK-

KQIVLQTVKDVFLQSLVDDNIVKTEK 62

Query: 65 IGTSNYYWAFPSKALHARKHKLEVLESQALSEGSQKHASLQKSIEKAKIGR--
 --CETEER 120

IGTSNYYW+FPS A +R+ L L++QL + QK +L ++I K R

E +

Sbjct: 63

IGTSNYYWFSFSDAKRSRESVLGSLQAQLDDLKQKSKTLDENISFEKSKRDNEGTEENDAN
 122

Query: 121

TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVVEEIRQANKVAKEAANRWTDNIFAISWA
 180

+ L + + + LK ++ C+P+ E + K EAAN WTD

I + ++

Sbjct: 123

QYTLELLHAKESLKLKLTQLSNLNHCNPETFELKNENTKKYMEAAANLWTDQIHTLIAFC
 182

Query: 181 KRKFGFEENKIDRTFGIPEDFD 202

R G + N+I IPED D

Sbjct: 183 -RDMGADTNQIREYCSIPEDLD 203

Figure 5A
121P1F1 Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

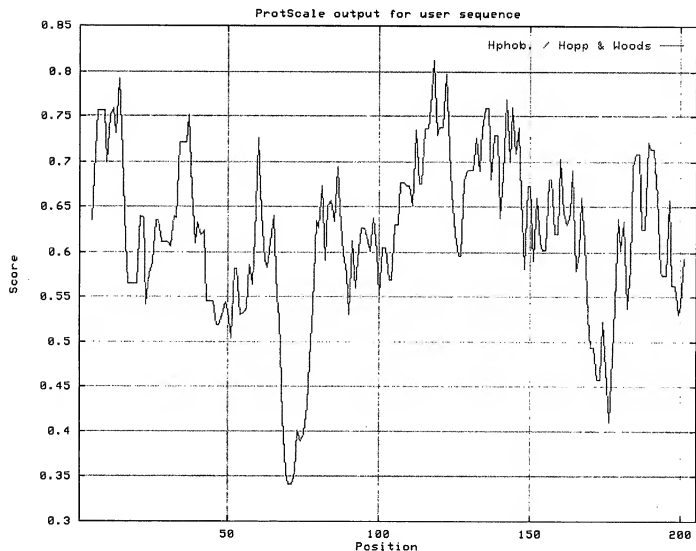


Figure 5B
121P1F1 variant 1a Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

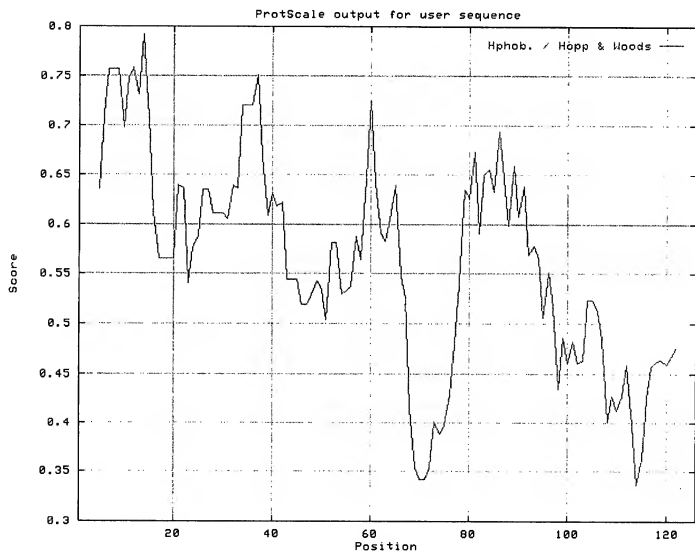


Figure 6A
121P1F1 Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

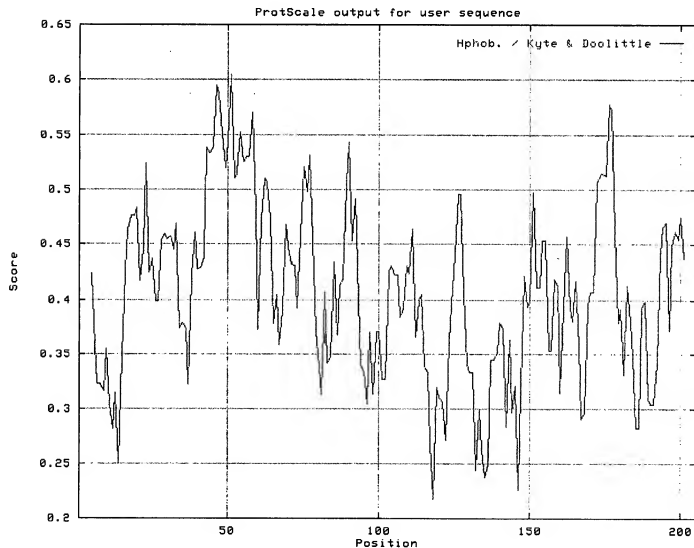


Figure 6B
121P1F1 variant 1a Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

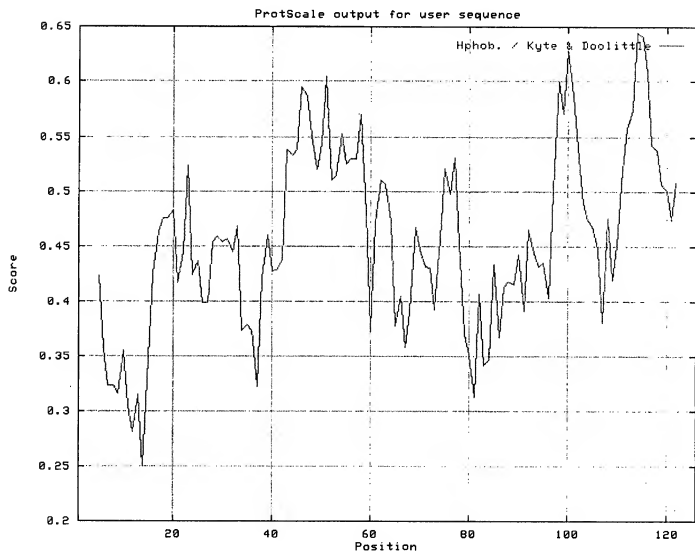


Figure 7A
121P1F1 % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

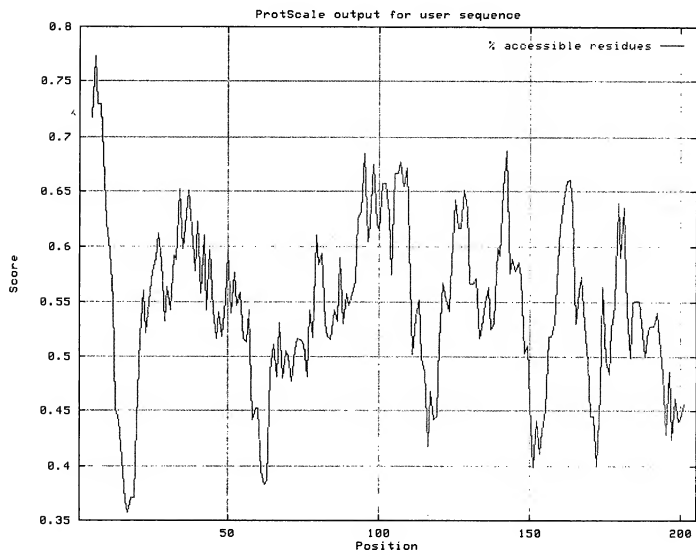


Figure 7B
121P1F1 variant 1a % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

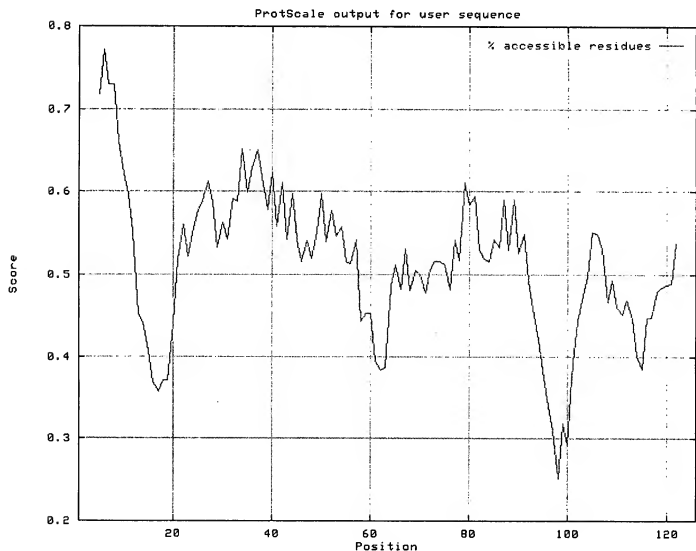


Figure 8A
121P1F1 Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

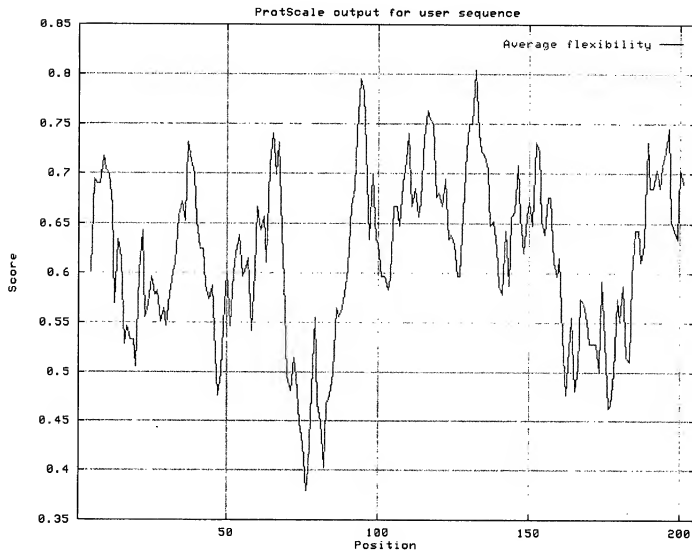


Figure 8B
121P1F1 variant 1a Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

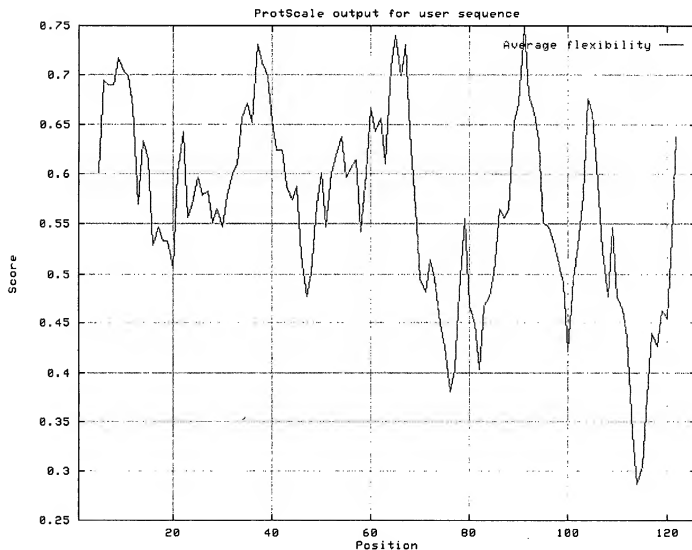


Figure 9A
121P1F1 Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

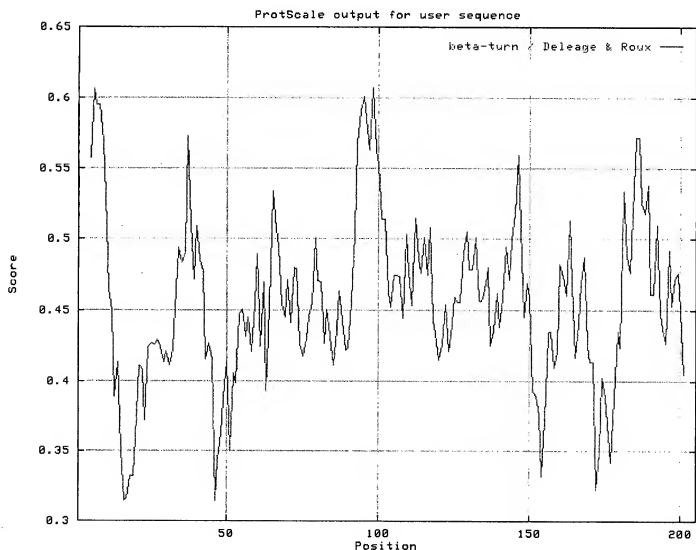


Figure 9B
121P1F1 variant 1a Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

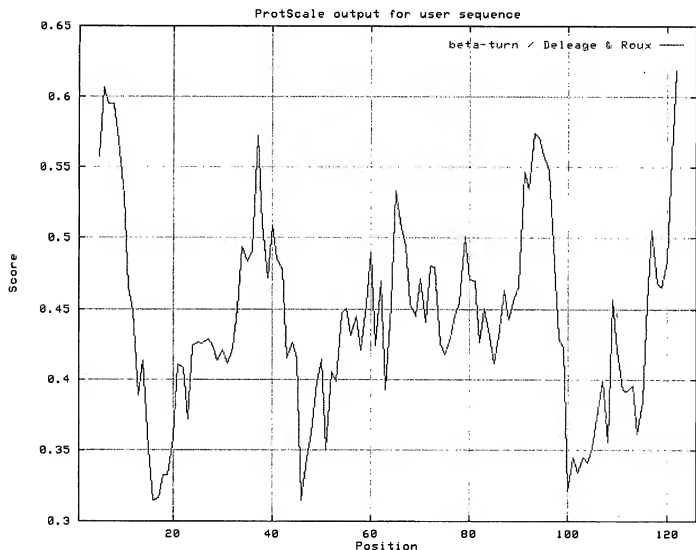
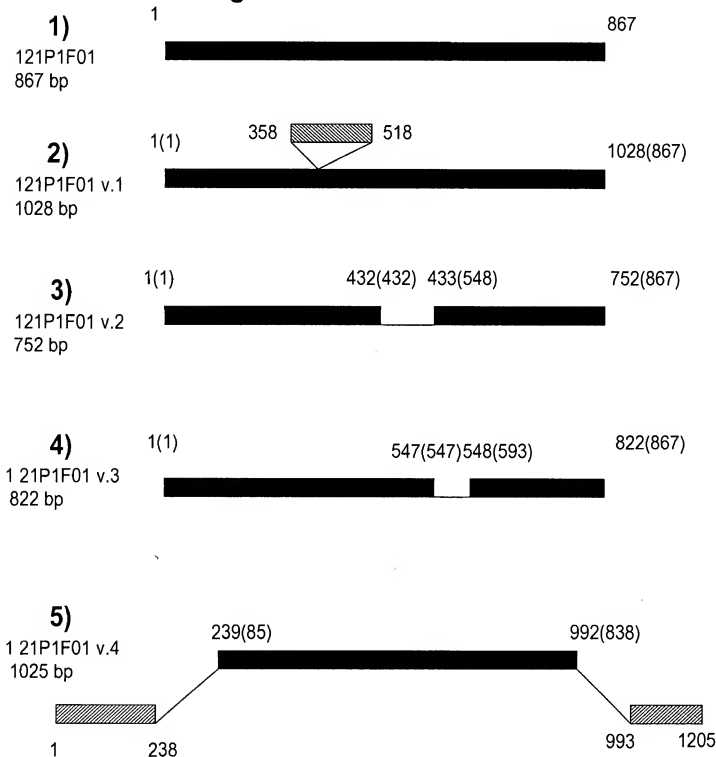
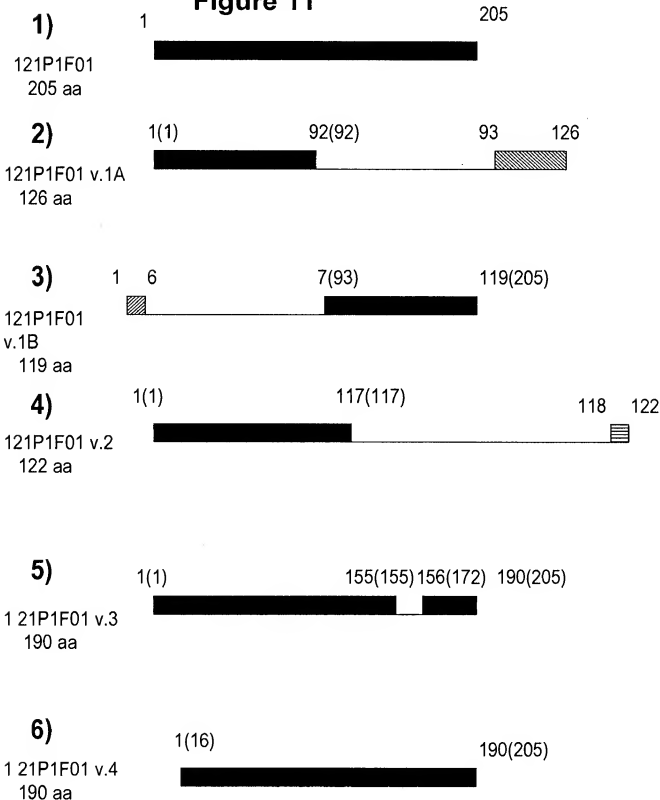


Figure 10



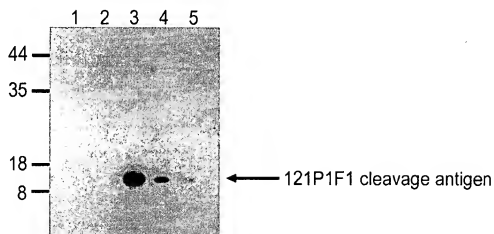
Note: Numbers in "()" correspond to those of the original sequence. Black box shows the same sequence as the original one. SNPs are indicated above the box.

Figure 11

Note: Numbers in "()" correspond to those of the original sequence. Black box shows the same sequence as the original one. Single amino acid variations are indicated above the box.

Figure 12

Specific recognition of 121P1F1 antigen by anti-121P1F1 pAb



1. Pre-immune	1:100
2. Pre-immune	1:1,600
3. Anti-121P1F1 serum	1:100
4. Anti-121P1F1 serum	1:400
5. Anti-121P1F1 serum	1:1,600

Figure 13

Expression of 121P1F1 in various cancer cells

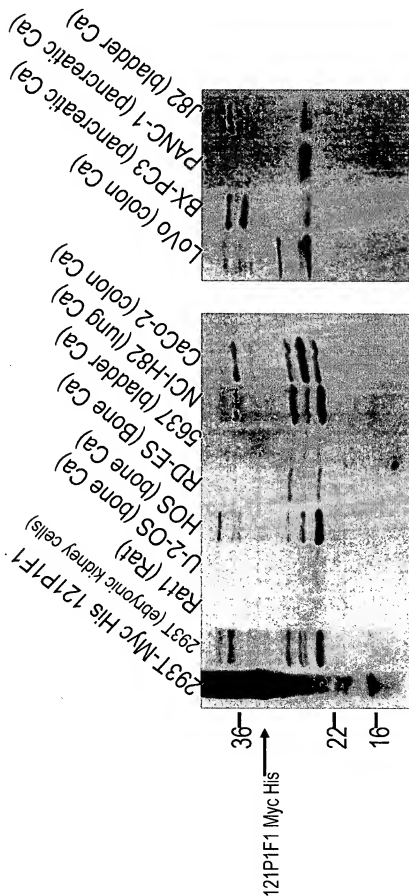


Figure 14 Expression of epitope tagged 121P1F1 in 293T cells

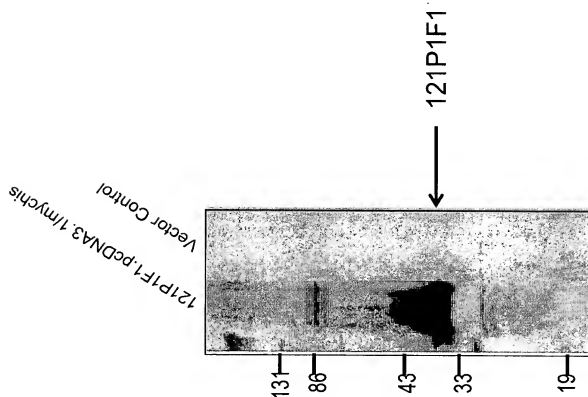
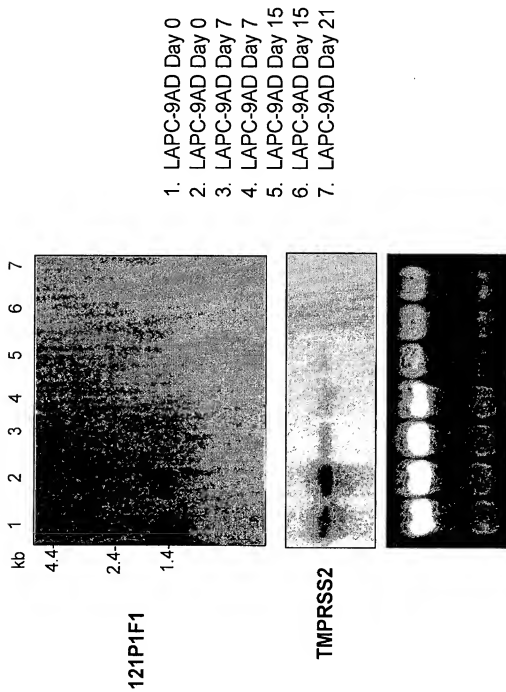
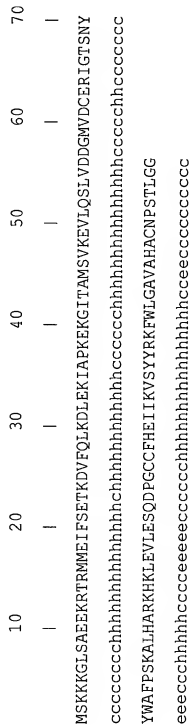


Figure 15 121P1F1 Androgen Regulation *In Vivo*



Alpha helix (h) : 61.95% Extended strand (e) : 1.95% Random coil (c) : 36.10%

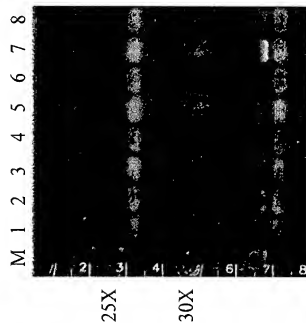
Figure 16B



Alpha helix (h) : 50.79% Extended strand (e) : 7.94% Random coil (c) : 41.27%

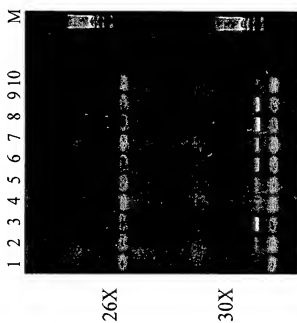
Figure 17 Expression of 121P1F1 by RT-PCR

A. Human normal tissues



- 1) Colon
- 2) Ovary
- 3) Leuk.
- 4) Prost.
- 5) Small Int.
- 6) Spleen
- 7) Testis
- 8) Thymus

B. Patient tumor specimens



- 1) VP1
- 2) VP2
- 3) XP
- 4) Normal prostate
- 5) Prostate cancer pool
- 6) Bladder cancer pool
- 7) Kidney cancer pool
- 8) Colon cancer pool
- 9) Lung tumor
- 10) H2O

Figure 18 Expression of 121P1F1 in normal human tissues

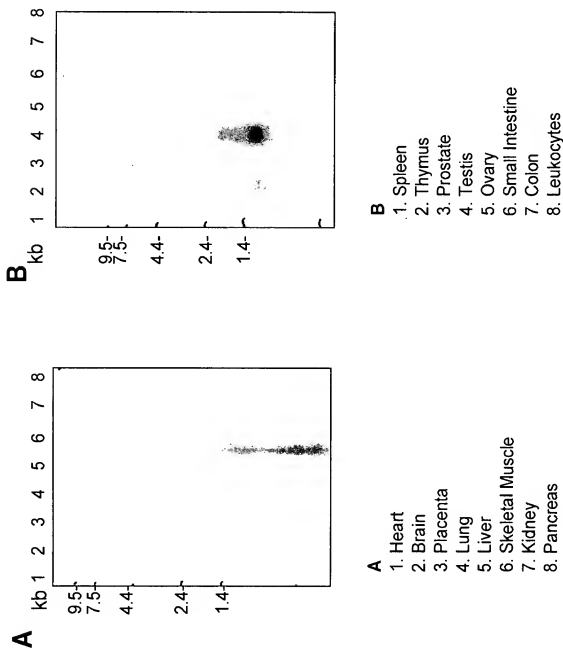
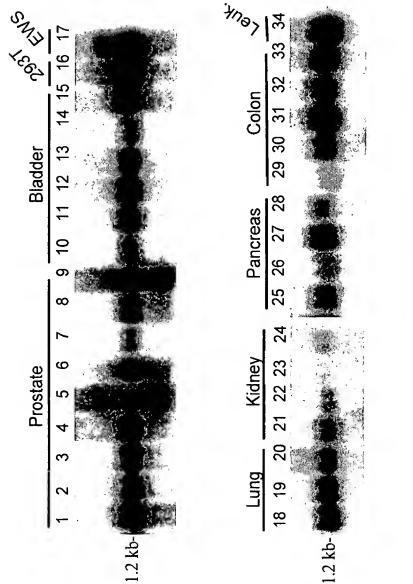
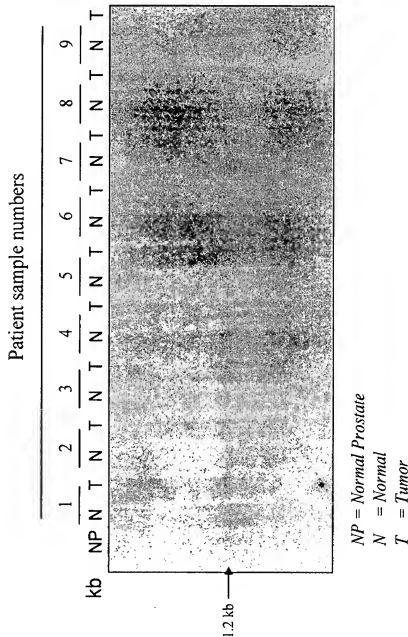


Figure 19 Expression of 121P1F1 in Multiple Cancer Cell lines



- | | |
|-------------|--------------|
| 1. LAPC 4AD | 18. A427 |
| 2. LAPC 4AI | 19. NCI-H82 |
| 3. LAPC 9AD | 20. NCI-H146 |
| 4. LAPC 9AI | 21. 769-P |
| 5. LNCaP | 22. A-498 |
| 6. PC-3 | 23. CAKI-1 |
| 7. DU145 | 24. SW 839 |
| 8. Tsu-Pr 1 | 25. PANC-1 |
| 9. LAPC 4 | 26. Bx PC-3 |
| 10. HT1197 | 27. HPAC |
| 11. SCaBER | 28. Capan-1 |
| 12. UM-UC-3 | 29. SK-CO-1 |
| 13. TCCSUP | 30. Caco-2 |
| 14. J82 | 31. LoVo |
| 15. 5637 | 32. T84 |
| 16. 293T | 33. Colo205 |
| 17. RD-ES | 34. KCL 22 |

Figure 20 Expression of 121P1F1 in Patient Prostate Cancer Samples



**Figure 21 Expression of 121P1F1 in Kidney, Breast,
 Cervical and Stomach Patients Samples as well as
 Cancer Cell lines**



T = tumor RNA

N = normal adjacent tissue RNA

Cancer cell lines are:
 (from left to right)

Cell Lines



HeLa (cervical carcinoma)
 Daudi (Burkitt's lymphoma)
 K562 (CML)
 HL-60 (PML)
 G361 (melanoma)
 A549 (lung carcinoma)
 MOLT-4 (lymphoblastic leuk.)
 SW480 (colorectal carcinoma)
 Raji (Burkitt's lymphoma)

Figure 22 Androgen Regulation of 121P1F1

